

D1
case 12

UAS_{GCN4p}: TGA_{CTCA}, and the TI box (SEQ ID NO:59):
CTCTTAAGTGCAAGTGACTGCGA, which also functions
as the binding site for the arginine repressor, argR.

In accordance with 37 C.F.R. § 1.121(b), also enclosed, in Appendix A, is a version of the above replacement paragraph marked up to show all the changes relative to the deleted paragraph.

On pages 17-18, delete last paragraph beginning on page 17, line 36, and ending on page 18, at line 4, and substitute for it the following replacement paragraph:

D2

When these additional motives are included, one arrives at the following 53 nucleobase degenerated sequence for an efficient promoter in *L. lactis*. Out of these 53 nucleobases, 34 bases are conserved two are semi-conserved (R and W) and 17 are allowed to vary randomly between the four nucleobases, SEQ ID NO:60:

In accordance with 37 C.F.R. § 1.121(b), also enclosed, in Appendix A, is a version of the above replacement paragraph marked up to show all the changes relative to the deleted paragraph.

On page 23, delete third paragraph beginning at line 10, and ending at line 16, and substitute for it the following replacement paragraph:

D3

This example illustrates the development of a temperature regulated promoter library for *L. lactis*. A regulatory element comprising an eight basepair inverted repeat that has been shown to be involved in the heatshock response of *L. lactis* is inserted a few base pairs upstream of the -35 sequence. The minimal extent of such a regulatory element seems to be 27 basepairs, SEQ ID NO:61:

In accordance with 37 C.F.R. § 1.121(b), also enclosed, in Appendix A, is a version of the above replacement paragraph marked up to show all the changes relative to the deleted paragraph.

On page 24, second paragraph beginning at line 18, and ending at line 23, and substitute for it the following replacement paragraph:

DU
When these sequences are combined, one arrives at the following 73 bp consensus sequence for a temperature regulated promoter in *L. lactis*. Out of these 73 bp, 45 are conserved, two are semi-conserved (R and W) and 26 are allowed to vary randomly between the four nucleobases, SEQ ID NO:62:

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In accordance with 37 C.F.R. § 1.121(b), also enclosed, in Appendix A, is a version of the above replacement paragraph marked up to show all the changes relative to the deleted paragraph.

IN THE CLAIMS:

Please amend claims 24 and 53. A clean version of the amended claims is set forth below. In accordance with 37 CFR § 1.121(b), also enclosed, in Appendix B, is a marked up version of these claims to show amendments made in them:

NE. 2
24. (Once Amended) An artificial promoter library according to claim 23, wherein said consensus sequences comprise the TATA box: TATAAA, the UAS_{GCN4p}: TGACTCA, and the TI box (SEQ ID NO:59): CTCTTAAGTGCAAGTGACTGCGA, which also functions as the binding site for the arginine repressor, argR.

NE. 2
53. (Once Amended) A method according to claim 52, wherein said consensus sequences comprise the TATA box: TATAAA, the the UAS_{GCN4p}: TGACTCA, and the TI box (SEQ ID NO:59): CTCTTAAGTGCAAGTGACTGCGA, which also functions as the binding site for the arginine repressor, argR.

REMARKS

In addition to the above amendment of the specification and further in response to the Notice to Comply, Applicants submit herewith a copy of the Substitute Sequence Listing in computer readable form, as required by 37 C.F.R. 1.821(e). The undersigned